

LISTING OF THE CLAIMS

1.-4. (Cancelled)

5. (Withdrawn-Currently Amended) A computer-readable medium carrying a microsatellite polymorphic marker distribution map and one or more sequences of instructions from a user of a computer system for analyzing said markers over a desired human genomic region, wherein the distribution map comprises information regarding the position of microsatellite polymorphic markers over one or more regions of the human genome, said markers being positioned at intervals of from about 50 Kb to 150 Kb, wherein execution of one or more sequences of instructions by one or more processors causes the one or more processors to perform a method, comprising:

receiving a query inputted by the user and receiving instructions as to a microsatellite markers or a human genomic region to include in analysis;

accessing distribution map information stored on the medium;

displaying a map showing the position of markers on a human genomic region, wherein the map provides at least the selected markers or markers within the selected region.

6. (Withdrawn) The computer-readable medium of claim 5, wherein the medium additionally carries sequence information for the markers.

7. (Withdrawn) The computer-readable medium of claim 6, wherein the sequence information comprises nucleotide sequences of SEQ ID NOS: 1-27088.

8. (Withdrawn-Currently Amended) An isolated polynucleotide useful as a primer, the polynucleotide being about 15 to 100 nucleotides in length and containing a nucleotide sequence extending in the 3'-direction from the 5'-terminus of a sequence of one of SEQ ID NOS: 1- 27088 or a nucleotide sequence complementary to a sequence extending in the 5'-direction from the 3'-terminus of a sequence of one of SEQ ID NOS: 1- 27088.

9. (Withdrawn) A method of assessing susceptibility of a human subject to psoriasis vulgaris, the method comprising:

analyzing a region of about 111 kb extending from C1_2_6 to C2_4_4 for the presence of a marker that is associated with psoriasis vulgaris, wherein the marker is allele 303, allele 357, allele 255, allele 259, or allele 223;

wherein detection of the marker is indicative of susceptibility of the subject to psoriasis vulgaris.

10. (Withdrawn-Currently Amended) The method of claim 9, wherein the marker is allele 303.

11. (Withdrawn-Currently Amended) The method of claim 9, wherein the subject is heterozygous and is identified as a carrier for psoriasis vulgaris.

12. (Withdrawn) The method of claim 9, wherein the subject is homozygous, and is susceptible to onset or has psoriasis vulgaris.

13. (Currently Amended) A gene mapping method, comprising:

selecting a combination of DNA sequences comprising SEQ ID Nos. 1-27088;

collecting DNA samples from affected subjects and control subjects;

performing polymerase chain reactions (PCR) using forward primers having a length of 15 to 100 nucleotides and having the same nucleotide sequence as the sequence extending in the 3'-direction from the 5'-terminus of each of the DNA sequences of said combination and reverse primers having a length of 15 to 100 nucleotides and having a nucleotide sequence complementary to the sequence extending in 5'-direction from the 3'-terminus of each of the DNA sequences of said combination to produce DNA sequence fragments; wherein each of the fragments includes a microsatellite genetic polymorphism marker;

analyzing alleles of the microsatellite genetic polymorphism markers of said DNA sequence fragments; and

statistically comparing allele frequencies observed in the DNA sequence fragments produced from the affected subjects with those observed in the DNA sequence fragments produced from the control subjects to identify microsatellite polymorphism markers found positive whose allele

frequencies observed in the DNA sequence fragments produced from the affected subjects are statistically significantly different from allele frequencies observed in their corresponding DNA sequence fragments produced from the control subjects, wherein the DNA fragments comprising at least one microsatellite polymorphism marker found positive are regarded as a region in which a pathogenic gene or a gene relating to human phenotypes associated with a genetic factor may exist.

~~the DNA sequence fragments of the affected subjects with the DNA sequence fragments of the control subjects to identify an existing region of a pathogenic gene or a gene relating to human phenotypes associated with a genetic factor.~~

14. (Currently Amended) The method according to claim 13, further comprising the step of mixing the DNA samples obtained from the affected subjects to provide pooled samples for affected subjects and mixing the DNA samples obtained from the control subjects to provide pooled DNA samples for control subjects before performing the polymerase chain reaction.

15. (Previously Presented) The method according to claim 13, wherein the DNA sequence fragments produced by PCR comprise all or a part of the DNA sequences of SEQ ID Nos: 1-27088.

16. (Currently Amended) The method according to claim 13, wherein said analyzing of alleles of the microsatellite genetic polymorphism markers ~~comparing~~ is carried out using a DNA chip and a mass spectrometer.

17. (Currently Amended) A gene mapping method according to claim 13, further comprising: selecting secondary DNA sequences containing at least one microsatellite polymorphism marker found positive through the method of claim 13 from the combination of DNA sequences comprising SEQ ID Nos. 1-27088;

collecting DNA samples from affected subjects different from the affected subjects of claim 13 and control subjects different from the control subjects of claim 13;

performing polymerase chain reaction (PCR) using forward primers having a length of 15 to 100 nucleotides and having the same nucleotide sequence as the sequence extending in the 3'-direction from the 5'-terminus of each of the secondary DNA sequences and reverse primers having a length of 15 to 100 nucleotides and having a nucleotide sequence complementary to the sequence extending in the 5'-

direction from the 3'-terminus of each of the secondary DNA sequences to produce secondary DNA sequence fragments;

analyzing alleles of the microsatellite genetic polymorphism markers of said secondary DNA sequence fragments, and

statistically comparing allele frequencies observed in the secondary DNA sequence fragments produced from the affected subjects with those observed in the secondary DNA sequence fragments produced from the control subjects to identify microsatellite polymorphism markers found true-positive whose allele frequencies observed in the secondary DNA sequence fragments produced from the affected subjects are statistically significantly different from allele frequencies observed in their corresponding secondary DNA sequence fragments produced from the control subjects, wherein the secondary DNA fragments comprising at least one microsatellite polymorphism marker found true-positive are regarded as a region in which a pathogenic gene or a gene relating to human phenotypes associated with a genetic factor exists with higher probability.

~~performing a second screening of DNA sequences comprising the microsatellite genetic polymorphism markers found positive through the method of claim 13 using DNA samples obtained from different affected subjects and the control subjects.~~

18. (Currently Amended) A gene mapping method according to claim 13, further comprising:
selecting secondary DNA sequences containing at least one microsatellite polymorphism marker found positive through the method of claim 13 from the combination of DNA sequences comprising SEQ ID Nos. 1-27088;

collecting DNA samples from descent groups having a pathogenic gene of an affected subject or a gene relating to a human phenotype with genetic factors;

performing polymerase chain reactions (PCR) using forward primers having a length of 15 to 100 nucleotides and having the same nucleotide sequence as the sequence extending in the 3'-direction from the 5'-terminus of each of the secondary DNA sequences and reverse primers having a length of 15 to 100 nucleotides and having a nucleotide sequence complementary to the sequence extending in the 5'-direction from the 3'-terminus of each of the secondary DNA sequences to produce secondary DNA sequence fragments;

analyzing alleles of the microsatellite genetic polymorphism markers of said secondary DNA sequence fragments, and

statistically comparing allele frequencies observed in the secondary DNA sequence fragments produced from the affected subjects with those observed in the DNA sequence fragments produced from the control subjects in the method of claim 13 to identify microsatellite polymorphism markers found true-positive whose allele frequencies observed in the secondary DNA sequence fragments produced from the descent group are statistically significantly different from allele frequencies observed in their corresponding DNA sequence fragments produced from the control subjects, wherein the secondary DNA fragments comprising at least one microsatellite polymorphism marker found true-positive are regarded as a region in which a pathogenic gene or a gene relating to human phenotypes associated with a genetic factor exists with higher probability.

~~performing a genetic analysis on each group of the DNA sequences comprising the microsatellite genetic polymorphism markers found positive through the method of claim 13 using DNA samples obtained from a descent group having a pathogenic gene of affected subjects or a gene relating to human phenotypes with genetic factors; and~~

~~identifying a region of the DNA sequence including the microsatellite genetic polymorphism markers that are found true-positive.~~

19. (Currently Amended) ~~A gene mapping~~ The method according to claim 13, further comprising:

analyzing said DNA sequence fragments comprising at least one microsatellite polymorphism marker found positive through the method of claim 13, based on allele frequency of known single nucleotide polymorphisms.

~~an existing candidate DNA segment based on single nucleotide polymorphisms, wherein said candidate DNA segment includes a pathogenic gene or a gene relating to human phenotypes with genetic factors and wherein the candidate DNA segment was identified by the method according to claims 13, 14, 17, or 18.~~

20. (New) The method according to claim 17 or 18, further comprising:

analyzing said DNA sequence fragments comprising at least one microsatellite polymorphism marker found true-positive through the method of claim 17 or 18, based on allele frequency of known single nucleotide polymorphisms.